

SEQUENCE LISTING

<110> Leproust, Eric M Wolber, Paul K.

<400> 5

<120> METHODS FOR IDENTIFYING SUITABLE NUCLEIC ACID PROBE SEQUENCES FOR USE IN NUCLEIC ACID ARRAYS

<130>	10030416-1	
	10/698,195 2003-10-30	
<160>	9	
<170>	FastSEQ for Windows Version 4.0	
<210><211><211><212><213>	16	
<400>		
atggac	ttag cattcg	16
<210> <211> <212> <213>	12	
<400>		
atggac	ttag ca	12
<210><211><211><212><213>	12	
<400>	3	
tggact	tagc at	12
<210><211><211><212><213>	12	
<400>		
ggactt	agca tt	12
<210><211><211><212><212><213>	12	

gacttagcat	LC			12
<210> 6 <211> 12 <212> DNA <213> homo	saniens			
	Dupions			
<400> 6				
acttagcatt	cg			12
<210> 7				
<211> 25				
<212> DNA				
<213> homo	sapiens			
	-			
<400> 7				
atcatcgtag	ctggtcagtg	tatcc		25
<210> 8				
<211> 25				
<212> DNA				
<213> homo	sapiens		•	
<400> 8				
	ctggtcagtg	+ > + = =		0.5
accatcytay	ciggicagig	tatte		25
<210> 9				
<211> 35				
<212> DNA				
<213> homo	sapiens			
	-			
<400> 9				
atcatcgtag	ctggtcagtg	tatccaaaaa	aaaaa	35